

## SEQUENCE LISTING

&lt;110&gt; UAB Research Foundation

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<120> METHODS AND COMPOSITIONS FOR IDENTIFYING  
COMPOUNDS THAT INHIBIT HIV-1 SUBUNIT-SPECIFIC REVERSE  
TRANSCRIPTASE

&lt;130&gt; 21085.0123P1

&lt;140&gt; Unassigned

&lt;141&gt; 2005-05-24

&lt;150&gt; 60/573,918

&lt;151&gt; 2004-05-24

&lt;150&gt; 60/668,858

&lt;151&gt; 2005-04-06

&lt;160&gt; 21

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 858

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

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<400> 1
gtttaaacgc caccatggag caggcccccg aggaccaggg cccccagagg gagccccaca      60
acgagtggac cctggagctg ctggaggagc tgaagaggga ggccgtgagg cacttccccca      120
ggccctggct gcaaggcctg ggccagcaca tctacgagac ctacggcgac acctgggccc      180
gcgtggaggc catcatcagg atcctgcagc agctgctgtt catccacttc aggatcgggc      240
gccagcacag caggatcgcc atcatccagc agaggagggc caggagggaac ggcgccagca      300
ggagctagtt taaacactgc acagagagac aggtctaatt tttagggaaa atttggcctt      360
ccaaacaaag gaggccaggg aattttctcc agaacaggcc agagcccaac gcccccaccg      420
cagagagcct cgggttcgga gaggagatag cccctcccc gaaacaagag ccgaaggaaa      480
aggagtata ccccttaacc tccctcaaat cactcttgg cagcgacccc tagtcacagt      540
aagaataggg ggacagctaa tagaagccct gttagacaca ggagcagatg atacagtgtt      600
agaagatata aatttaccag gaaaatggaa accaaaaatg atagggggaa ttggtggctt      660
tatcaaatga agacagtatg atcaaatact tatagaaatt tgtggaaaaa aggcctatagg      720
gacagtatta gtaggaccta cacttatcaa cataattggg agaaatatgt tgactcagat      780
tggtgttact ttaaattttc caattagtc tattgaaact gtaccagtaa aattaaagcc      840
aggaatggat ggtccaaa

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&lt;210&gt; 2

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 2

Met	Glu	Gln	Ala	Pro	Glu	Asp	Gln	Gly	Pro	Pro	Arg	Glu	Pro	Tyr	Asn
1				5					10					15	
Ala	Trp	Thr	Leu	Glu	Leu	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Ala	Val	Arg
			20					25				30			
His	Phe	Pro	Arg	Val	Trp	Leu	His	Gly	Leu	Gly	Gln	His	Ile	Tyr	Glu
		35				40					45				
Thr	Tyr	Gly	Asp	Thr	Trp	Ala	Gly	Val	Glu	Ala	Ile	Ile	Arg	Ile	Leu
	50				55					60					
Gln	Gln	Leu	Leu	Phe	Ile	His	Phe	Arg	Ile	Gly	Cys	Gln	His	Ser	Arg
65				70					75				80		
Ile	Gly	Ile	Thr	Arg	Gln	Arg	Arg	Ala	Arg	Asn	Gly	Ala	Ser	Arg	Ser
			85					90					95		

<210> 3

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 3

gtttaaacgc	caccatggag	caggcccccg	aggaccaggg	ccccagagg	gagccccaca	60
acgagtgga	cctggagctg	ctggaggagc	tgaagagga	ggcctgagg	cacttcccc	120
ggccctggct	gcacggcctg	ggccagcaca	tctacgagac	ctacggcgac	acctgggccc	180
gcgtggaggc	catcatcagg	atcctgcagc	agctgctgtt	catccacttc	aggatcggct	240
gccagcacag	caggatcggc	atcatccagc	agaggagggc	caggaggaac	ggcgcacgca	300
ggagctagtt	taaac					315

<210> 4

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 4

Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met
1				5				10					15		
Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys
			20					25				30			
Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser
		35				40					45				
Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys
	50				55					60					
Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu
65				70					75				80		
Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His
		85						90					95		
Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly
		100						105					110		
Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr
		115						120					125		

Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr  
 130 135 140  
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe  
 145 150 155 160  
 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro  
 165 170 175  
 Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp  
 180 185 190  
 Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His  
 195 200 205  
 Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu  
 210 215 220  
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr  
 225 230 235 240  
 Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp  
 245 250 255  
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro  
 260 265 270  
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala  
 275 280 285  
 Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala  
 290 295 300  
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp  
 305 310 315 320  
 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln  
 325 330 335  
 Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly  
 340 345 350  
 Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu  
 355 360 365  
 Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly  
 370 375 380  
 Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr  
 385 390 395 400  
 Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe  
 405 410 415  
 Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu  
 420 425 430  
 Pro Ile Val Gly Ala Glu Thr Phe  
 435 440

&lt;210&gt; 5

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 5

Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met  
 1 5 10 15  
 Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys  
 20 25 30  
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser  
 35 40 45  
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys  
 50 55 60  
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu  
 65 70 75 80

```

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
      85                      90                      95
Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
      100                    105                    110
Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
      115                    120                    125
Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
      130                    135                    140
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
      145                    150                    155                    160
Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
      165                    170                    175
Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
      180                    185                    190
Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His
      195                    200                    205
Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu
      210                    215                    220
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
      225                    230                    235                    240
Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
      245                    250                    255
Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro
      260                    265                    270
Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
      275                    280                    285
Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
      290                    295                    300
Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
      305                    310                    315                    320
Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
      325                    330                    335
Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
      340                    345                    350
Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
      355                    360                    365
Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
      370                    375                    380
Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
      385                    390                    395                    400
Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
      405                    410                    415
Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu
      420                    425                    430
Pro Ile Val Gly Ala Glu Thr Phe
      435                    440

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&lt;210&gt; 6

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 6

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Lys Glu Gly His Gln Met Lys Glu Cys Thr Glu Arg Gln Ala Asn Phe
  1                      5                      10                      15
Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu
      20                      25                      30

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Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe	Arg	Cys	
		35					40					45				
Gly	Glu	Glu	Lys	Thr	Thr	Pro	Pro	Gln	Lys	Pro	Glu	Gln	Thr	Asp	Lys	
		50				55				60						
Glu	Leu	Tyr	Pro	Leu	Ala	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Gln	Arg	Pro	
65				70					75					80		
Leu	Val	Thr	Ile	Lys	Ile	Gly	Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	
			85					90					95			
Thr	Gly	Ala	Asp	Asp	Thr	Val	Leu	Glu	Asp	Met	Ser	Leu	Pro	Gly	Lys	
		100					105						110			
Trp	Lys	Pro	Lys	Met	Ile	Gly	Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	
		115				120					125					
Gln	Tyr	Asp	Gln	Ile	Pro	Ile	Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	
	130			135					140							
Thr	Val	Leu	Ile	Gly	Pro	Thr	Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	
145				150					155					160		
Leu	Thr	Gln	Ile	Gly	Cys	Thr	Leu	Asn	Phe							
			165					170								

&lt;210&gt; 7

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 7

aaaggaagga	caccaaatga	aagaatgcac	tgagagacag	gctaattttt	tagggaaaat	60
ctggccttcc	cacaagggaa	ggccagggaa	ctttctccag	agcagaccag	agccaacagc	120
ccaccagaaa	gagagcttca	ggtgtgggga	ggagaaaaa	actccccctc	agaagccgga	180
gcagacagac	aaggaaactgt	atccttttagc	ttccctcaga	tcactctttg	gcaacgaccc	240
ctcgtcacaa	taaagataggt	ggggcagcta	aaggaagctc	tattagatac	aggagcagat	300
gatacagtat	tagaagacat	gagtttgcca	ggaaaaatgga	agccaaaaat	gatatggggga	360
attggagggtt	ttatcaaagt	aagacagtat	gatcagatac	ctatagaaat	ctgtgggcat	420
aaagctatag	gtacagtatt	aataggacca	acacctgtca	acataattgg	aagaaatctg	480
ttgacacaga	ttggttgcat	tttaaatatt	c			511

&lt;210&gt; 8

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 8

Tyr Met Asp Asp  
1

&lt;210&gt; 9

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

<220>  
 <221> VARIANT  
 <222> 2  
 <223> Xaa = any amino acid  
  
 <400> 9  
 Tyr Xaa Asp Asp  
 1  
  
 <210> 10  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct  
  
 <400> 10  
 aagccccgga tggatggccc aaaagt 26  
  
 <210> 11  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct  
  
 <400> 11  
 tcctaaacgc gtctccctct aagctgctca atttacttag aaagt 45  
  
 <210> 12  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct  
  
 <400> 12  
 actttctaag taaattgagc agcttagagg gagacgcgtt tagga 45  
  
 <210> 13  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct  
  
 <400> 13  
 tatgtcgaca cccaattatg aaaag 25  
  
 <210> 14  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence; note =
        synthetic construct

<400> 14
tagatcagat ctgttgactc agattgggtg ca
32

<210> 15
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
        synthetic construct

<400> 15
atctacacgc gtttagaagg tttctgcgcc tt
32

<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
        synthetic construct

<400> 16
ttattaaacgc gtccgccct ctccctcccc cc
32

<210> 17
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
        synthetic construct

<400> 17
ccatcccggt ctttaatttt actggtacag tttcaatagg actaatgggt cccatgggtat
60
tactgtctt
69

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
        synthetic construct

<400> 18
agcttgccctt gactgcttca a
21

<210> 19
<211> 26
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 19

ctgctagaga ttttccacac tgacta

26

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 20

ggctagctag ggaaccact g

21

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 21

atactgacgc tctcgaccc at

22